



SEQUENCE LISTING

<110> Reinherz, Ellis L.
Freund, Christian
Li, Jing
Nishizawa, Kazuhisa
Wagner, Gerhard

<120> Cloning and Characterization of a CD2
Binding Protein (CD2BP2)

<130> 1062.1021-004

<140> US 09/873,106

<141> 2001-06-01

<150> US 60/111,007

<151> 1998-12-04

<150> US 60/115,647

<151> 1999-01-13

<150> PCT/US99/26993

<151> 1999-11-15

<160> 25

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1299

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (121)...(1143)

<400> 1

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tcttttttcc acctgcctt ccgcggattc ccagcttgag aaacacctct ttgccccgtc 120
atg cca aag agg aaa gtg acc ttc caa ggc gtg gga gat gag gag gat 168
Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp
1 5 10 15

gag gat gaa atc att gtc ccc aag aag aag ctg gtg gac cct gtg gct 216
Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala
20 25 30

ggg tca ggg ggt cct ggg agc cgc ttt aaa ggc aaa cac tct ttg gat 264
Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp
35 40 45

agc gat gag gag gag gat gat gat gat ggg ggg tcc agc aaa tat gac 312
Ser Asp Glu Glu Glu Asp Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp
50 55 60

| | |
|---|------|
| atc ttg gcc tca gag gat gta gaa ggt cag gag gca gcc aca ctc ccc Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro 65 70 75 80 | 360 |
| agc gag ggg ggt ggt cgg atc aca ccc ttt aac ctg cag gag gag atg Ser Glu Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met 85 90 95 | 408 |
| gag gaa ggc cac ttt gat gcc gat ggc aac tac ttc ctg aac cgg gat Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp 100 105 110 | 456 |
| gct cag atc cga gac agc tgg ctg gac aac att gac tgg gtg aag atc Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile 115 120 125 | 504 |
| cgg gag cgg cca cct ggc cag cgc cag gcc tca gac tcg gag gag gag Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu 130 135 140 | 552 |
| gac agc ttg ggc cag acc tca atg agt gcc caa gcc ctc ttg gag gga Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly 145 150 155 160 | 600 |
| ctt ttg gag ctc cta ttg cct aga gag aca gtg gct ggg gca ctg agg Leu Leu Glu Leu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg 165 170 175 | 648 |
| cgt ctg ggg gcc cga gga gga ggc aaa ggg aga aag ggg cct ggg caa Arg Leu Gly Ala Arg Gly Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln 180 185 190 | 696 |
| ccc agt tcc cct cag cgc ctg gac cgg ctc tcc ggg ttg gcc gac cag Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln 195 200 205 | 744 |
| atg gtg gcc cgg ggc aac ctt ggt gtg tac cag gaa aca agg gaa cgg Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg 210 215 220 | 792 |
| ttg gct atg cgt ctg aag ggt ttg ggg tgt cag acc cta gga ccc cac Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His 225 230 235 240 | 840 |
| aat ccc aca ccc cca ccc tcc ctg gac atg ttc gct gag gag ttg gcg Asn Pro Thr Pro Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala 245 250 255 | 888 |
| gag gag gaa ctg gag acc cca acc cct acc cag aga gga gaa gca gag Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu 260 265 270 | 936 |
| tcg cgg gga gat ggt ctg gtg gat gtg atg tgg gaa tat aag tgg gag Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu 275 280 285 | 984 |
| aac acg ggg gat gcc gag ctg tat ggg ccc ttc acc agc gcc cag atg Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met 290 295 300 | 1032 |

cag acc tgg gtg agt gaa ggc tac ttc ccg gac ggt gtt tat tgc cgg 1080
 Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg
 305 310 315 320

aag ctg gac ccc cct ggt ggt cag ttc tac aac tcc aaa cgc att gac 1128
 Lys Leu Asp Pro Pro Gly Gly Gln Phe Tyr Asn Ser Lys Arg Ile Asp
 325 330 335

ttt gac ctc tac acc tgagcctgct gggggcccag tttggtgggc ccttctttcc 1183
 Phe Asp Leu Tyr Thr
 340

tggactttgt ggaggaggca ccaagtgtct caggcagcga ggaaattgga ggccattttt 1243
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<210> 2

<211> 341

<212> PRT

<213> Homo sapiens

<400> 2

Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp
 1 5 10 15
 Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala
 20 25 30
 Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp
 35 40 45
 Ser Asp Glu Glu Glu Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp
 50 55 60
 Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro
 65 70 75 80
 Ser Glu Gly Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met
 85 90 95
 Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp
 100 105 110
 Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile
 115 120 125
 Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu
 130 135 140
 Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly
 145 150 155 160
 Leu Leu Glu Leu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg
 165 170 175
 Arg Leu Gly Ala Arg Gly Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln
 180 185 190
 Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln
 195 200 205
 Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg
 210 215 220
 Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His
 225 230 235 240
 Asn Pro Thr Pro Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala
 245 250 255
 Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu
 260 265 270
 Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu
 275 280 285

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Thr | Gly | Asp | Ala | Glu | Leu | Tyr | Gly | Pro | Phe | Thr | Ser | Ala | Gln | Met |
| 290 | | | | | | 295 | | | | | 300 | | | | |
| Gln | Thr | Trp | Val | Ser | Glu | Gly | Tyr | Phe | Pro | Asp | Gly | Val | Tyr | Cys | Arg |
| 305 | | | | | 310 | | | | | 315 | | | | 320 | |
| Lys | Leu | Asp | Pro | Pro | Gly | Gly | Gln | Phe | Tyr | Asn | Ser | Lys | Arg | Ile | Asp |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Phe | Asp | Leu | Tyr | Thr | | | | | | | | | | | |
| | | | 340 | | | | | | | | | | | | |

<210> 3
 <211> 26
 <212> PRT
 <213> Homo sapiens

| | | | | | | | | | | | | | | | |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 3 | | | | | | | | | | | | | | | |
| Gly | Asp | Ala | Glu | Leu | Tyr | Gly | Pro | Phe | Thr | Ser | Ala | Gln | Met | Gln | Thr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Trp | Val | Ser | Glu | Gly | Tyr | Phe | Pro | Asp | Gly | | | | | | |
| | | | 20 | | | | | 25 | | | | | | | |

<210> 4
 <211> 27
 <212> PRT
 <213> Caenorhabditis elegans

| | | | | | | | | | | | | | | | |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 4 | | | | | | | | | | | | | | | |
| Gly | Pro | Asp | Ser | Glu | Lys | Tyr | Gly | Pro | Tyr | Met | Ser | Lys | Asp | Met | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Phe | Trp | Leu | Gln | Ala | Gly | Tyr | Phe | Asn | Asp | Gly | | | | | |
| | | | 20 | | | | | 25 | | | | | | | |

<210> 5
 <211> 27
 <212> PRT
 <213> Caenorhabditis elegans

| | | | | | | | | | | | | | | | |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 5 | | | | | | | | | | | | | | | |
| Asp | Pro | Thr | Glu | Thr | Arg | Arg | Gly | Pro | Phe | Pro | Lys | Asp | Gln | Met | Asn |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Trp | Phe | Lys | Ala | Gly | Tyr | Phe | Thr | Asp | Glu | | | | | |
| | | | 20 | | | | | 25 | | | | | | | |

<210> 6
 <211> 27
 <212> PRT
 <213> Caenorhabditis elegans

| | | | | | | | | | | | | | | | |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 6 | | | | | | | | | | | | | | | |
| Asp | Asp | Arg | Gly | Thr | Val | Gln | Gly | Pro | Tyr | Gly | Ala | Ser | Thr | Val | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Asp | Trp | Tyr | Gln | Lys | Gly | Tyr | Phe | Ser | Asp | Asn | | | | | |
| | | | 20 | | | | | 25 | | | | | | | |

<210> 7

<211> 29
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 7
 Asp Thr Gln Gly Gln Ile His Gly Pro Phe Thr Thr Gln Met Met Ser
 1 5 10 15
 Gln Trp Tyr Ile Gly Gly Leu Glu Tyr Phe Ala Ser Thr
 20 25

<210> 8
 <211> 27
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 8
 Asp Ser Asn Gly Asn Ile Gln Gly Pro Phe Gly Thr Asn Asn Met Ser
 1 5 10 15
 Gln Trp Tyr Gln Gly Gly Tyr Phe Thr Pro Thr
 20 25

<210> 9
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Motif in CD2 binding region of CD2BP2

<221> VARIANT
 <222> 3, 4, 5, 6, 7, 8, 9, 10, 12, 13, 14
 <223> Xaa = Any Amino Acid

<400> 9
 Gly Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Gly Thr
 1 5 10 15
 Phe

<210> 10
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD2BP2 binding region

<400> 10
 Pro Pro Pro Gly His Arg
 1 5

<210> 11
 <211> 70

<212> PRT
 <213> Homo sapiens

<400> 11
 Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro
 1 5 10 15
 Pro Pro Pro Gly His Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro
 20 25 30
 Ala Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro
 35 40 45
 Arg Pro Arg Val Gln Pro Lys Pro Pro His Gly Ala Ala Glu Asn Ser
 50 55 60
 Leu Ser Pro Ser Ser Asn
 65 70

<210> 12
 <211> 8
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Kozak consensus sequence

<400> 12
 ccgccacc

8

<210> 13
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Flag Epitope

<400> 13
 gactacaagg acgacgatga caag

24

<210> 14
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Flag Epitope

<400> 14
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 15
 <211> 31
 <212> PRT
 <213> Gallus gallus

<220>
 <223> Flag Epitope

<400> 15

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Tyr | Tyr | Lys | Asp | Pro | Gln | Gly | Glu | Ile | Gln | Gly | Pro | Phe | Ser | Asn |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gln | Glu | Met | Ala | Glu | Trp | Phe | Gln | Ala | Gly | Tyr | Phe | Thr | Met | Ser | |
| | | | 20 | | | | | 25 | | | | | 30 | | |

<210> 16

<211> 38

<212> PRT

<213> *Drosophila melanogaster*

<220>

<223> Flag Epitope

<400> 16

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Thr | Trp | Glu | Phe | Lys | Trp | Ser | Gln | Asp | Glu | Thr | Asp | Ile | Gln |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gly | Pro | Phe | Ser | Thr | Glu | Lys | Met | Leu | Lys | Trp | Ser | Gln | Glu | Asn | Thr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Arg | Tyr | Phe | Lys | Asn | Gly | | | | | | | | | | |
| | | | 35 | | | | | | | | | | | | |

<210> 17

<211> 34

<212> PRT

<213> *Leishmania major*

<220>

<223> Flag Epitope

<400> 17

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Trp | Met | Met | Arg | Trp | Lys | Ala | Lys | Pro | Thr | Val | Gln | His | Gly | Pro |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Phe | Thr | Asp | Asp | Ala | Ile | Gln | Gln | Trp | Gly | Arg | Asp | Gly | Tyr | Phe | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Lys | Lys | | | | | | | | | | | | | | |

<210> 18

<211> 36

<212> PRT

<213> *Caenorhabditis elegans*

<220>

<223> Flag Epitope

<400> 18

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Asp | Thr | Lys | Trp | His | Tyr | Leu | Gly | Pro | Asp | Ser | Glu | Lys | Tyr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gly | Pro | Tyr | Met | Ser | Lys | Asp | Met | Leu | Phe | Trp | Leu | Gln | Ala | Gly | Tyr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Phe | Asn | Asp | Gly | | | | | | | | | | | | |
| | | | 35 | | | | | | | | | | | | |

<210> 19

<211> 35
 <212> PRT
 <213> *Caenorhabditis elegans*

<220>
 <223> Flag Epitope

<400> 19
 Val Glu Ser Ser Trp Arg Tyr Ile Asp Thr Gln Gly Gln Ile His Gly
 1 5 10 15
 Pro Phe Thr Ile Gln Met Met Ser Gln Trp Tyr Ile Gly Gly Tyr Phe
 20 25 30
 Ala Ser Thr
 35

<210> 20
 <211> 35
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<220>
 <223> Flag Epitope

<400> 20
 Ile Glu Ser Gln Trp Lys Tyr Ile Asp Ser Asn Gly Asn Ile Gln Gly
 1 5 10 15
 Pro Phe Gly Thr Asn Asn Met Ser Gln Trp Tyr Gln Gly Gly Tyr Phe
 20 25 30
 Thr Pro Thr
 35

<210> 21
 <211> 31
 <212> PRT
 <213> *Saccharomces pombe*

<220>
 <223> Flag Epitope

<400> 21
 Trp Leu Tyr Lys Asp Pro Gln Asn Asn Val Gln Gly Pro Phe Thr Gly
 1 5 10 15
 Val Asp Met His Gln Trp Tyr Arg Ala Gly Tyr Phe Pro Leu Gly
 20 25 30

<210> 22
 <211> 21
 <212> PRT
 <213> *Homo sapiens*

<220>
 <223> Flag Epitope

<400> 22
 Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro
 1 5 10 15

Pro Pro Gly His Arg
20

<210> 23
<211> 62
<212> PRT
<213> Homo sapiens

<220>
<223> Flag Epitope

<400> 23
Asp Val Met Trp Glu Tyr Lys Trp Glu Asn Thr Gly Asp Ala Glu Leu
1 5 10 15
Tyr Gly Pro Phe Thr Ser Ala Gln Met Gln Thr Trp Val Ser Glu Gly
20 25 30
Tyr Phe Pro Asp Gly Val Tyr Cys Arg Lys Leu Asp Pro Pro Gly Gly
35 40 45
Gln Phe Tyr Asn Ser Lys Arg Ile Asp Phe Asp Leu Tyr Thr
50 55 60

<210> 24
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<223> Flag Epitope

<400> 24
Trp Tyr Tyr Lys Asp Pro Gln Gly Glu Ile Gln Gly Pro Phe Asn Asn
1 5 10 15
Gln Glu Met Ala Glu Trp Phe Gln Ala Gly Tyr Phe Thr Met Ser
20 25 30

<210> 25
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<223> Flag Epitope

<400> 25
Gln Trp Phe Ser Arg Ser Leu Ala Pro Cys Pro Gly Pro Phe Thr Thr
1 5 10 15
Gln Glu Met Ala Glu Trp Phe Gln Ala Gly Tyr Phe Ser Met Ser
20 25 30